

10/559097

AP16 Rec'd PCT/PTO 01 DEC 2005  
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Monocotyledonous plants having improved growth characteristics  
and a method for making the same

<130> CD-097-PCT

<150> EP 03076719.8

<151> 2003-06-03

<160> 30

<170> PatentIn version 3.2

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<212> DNA

<213> Oryza sativa

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Glu	Ile	Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp
145					150				155						160
Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu
				165					170					175	
Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val
			180					185					190		

Val	Leu	Phe	Asn	Ala	Ile	Gln	Ser	Phe	Asp	Leu	Asn	Gln	Leu	Asn	Pro	195	200	205
Ser	Ile	Ala	Leu	His	Phe	Leu	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Val	Ala	210	215	220
Ser	Thr	Leu	Leu	Gly	Val	Val	Thr	Gly	Leu	Leu	Ser	Ala	Tyr	Val	Ile	225	230	235
Lys	Lys	Leu	Tyr	Ile	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu	245	250	255
Met	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Thr	Tyr	260	265	270
Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His	275	280	285
Tyr	Thr	Trp	His	Asn	Val	Thr	Gln	Ser	Ser	Arg	Ile	Thr	Thr	Lys	His	290	295	300
Ser	Phe	Ala	Thr	Leu	Ser	Phe	Val	Ala	Glu	Ile	Phe	Ile	Phe	Leu	Tyr	305	310	315
Val	Gly	Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Lys	Phe	Val	Ser	Asp	325	330	335
Ser	Pro	Gly	Thr	Ser	Ile	Ala	Ala	Ser	Ser	Val	Leu	Leu	Gly	Leu	Ile	340	345	350
Leu	Leu	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	355	360	365
Leu	Thr	Lys	Lys	Ser	Gln	His	Gln	Lys	Ile	Ser	Phe	Arg	Gln	Gln	Val	370	375	380
Ile	Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu	385	390	395
Ala	Tyr	Asn	Gln	Phe	Thr	Met	Ser	Gly	His	Thr	Gln	Leu	Arg	Ser	Asn	405	410	415
Ala	Ile	Met	Ile	Thr	Ser	Thr	Ile	Thr	Val	Val	Leu	Phe	Ser	Thr	Val	420	425	430
Val	Phe	Gly	Leu	Leu	Thr	Lys	Pro	Leu	Ile	Arg	Leu	Leu	Leu	Pro	His	435	440	445
Pro	Lys	Ile	Thr	Ser	Ser	Met	Thr	Thr	Thr	Glu	Ser	Thr	Thr	Pro	Lys	450	455	460
Ser	Phe	Ile	Val	Pro	Leu	Leu	Gly	Asp	Ser	Arg	Asp	Ser	Glu	Ala	Asp	465	470	475
Leu	Glu	Gly	His	Glu	Ile	His	Arg	Pro	Asn	Ser	Leu	Arg	Ala	Leu	Leu	485	490	495



Ser Thr Pro Thr His Thr Val His Arg Leu Trp Arg Lys Phe Asp Asp  
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Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Val Glu  
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Pro Gly Ser Pro Ser Glu Arg Asn Gly Asn Gln Trp Gly  
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<211> 2263  
<212> DNA  
<213> Suaeda maritima subsp. salsa

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<211> 556  
<212> PRT

<213> Suaeda maritima subsp. salsa

<400> 8

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Leu	Leu	Arg	Gly	Cys	Ile	Val	Ile	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg
		35					40					45			
Trp	Met	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Leu	Ile	Gly	Leu	Ser	Thr	Gly
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Ile	Ile	Ile	Leu	Leu	Ile	Ser	Gly	Gly	Lys	Ser	Ser	His	Leu	Leu	Val
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Phe	Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe
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Thr	Ile	Ile	Leu	Phe	Gly	Ala	Val	Gly	Thr	Leu	Val	Ser	Phe	Ile	Ile
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Ile	Ser	Leu	Gly	Ser	Ile	Ala	Ile	Phe	Gln	Lys	Met	Asp	Ile	Gly	Ser
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Asp	Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu
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Val	Val	Leu	Phe	Asn	Ala	Ile	Gln	Asn	Phe	Asp	Leu	Thr	His	Ile	Asp
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His	Arg	Ile	Ala	Phe	Gln	Phe	Gly	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Phe
	210					215					220				
Ala	Ser	Thr	Leu	Leu	Gly	Ala	Val	Thr	Gly	Leu	Leu	Ser	Ala	Tyr	Val
225					230					235					240
Ile	Lys	Lys	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala
			245						250					255	
Leu	Met	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe
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Tyr	Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser
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His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys  
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His Ala Phe Ala Thr Leu Ser Phe Val Ala Glu Ile Phe Ile Phe Leu  
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Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Arg Phe Val Ser  
325 330 335

Asp Ser Pro Gly Thr Ser Val Ala Val Ser Ser Ile Leu Leu Gly Leu  
340 345 350

His Met Val Gly Arg Ala Ala Phe Val Phe Pro Phe Ala Phe Leu Met  
355 360 365

Asn Leu Ser Lys Lys Ser Asn Ser Glu Lys Val Thr Phe Asn Gln Gln  
370 375 380

Ile Val Ile Trp Trp Ala Gly Leu Met Lys Ser Ala Val Ser Val Ala  
385 390 395 400

Leu Ala Tyr Asn Gln Phe Ser Arg Ser Gly His Thr Gln Leu Arg Gly  
405 410 415

Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr  
420 425 430

Met Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Leu Phe Met Leu Pro  
435 440 445

Gln Pro Lys His Phe Thr Ser Ala Ser Thr Val Ser Asp Leu Gly Ser  
450 455 460

Pro Lys Ser Phe Ser Leu Pro Leu Leu Glu Asp Arg Gln Asp Ser Glu  
465 470 475 480

Ala Asp Leu Gly Asn Asp Asp Glu Glu Ala Tyr Pro Arg Gly Thr Ile  
485 490 495

Ala Arg Pro Thr Ser Leu Arg Met Leu Leu Asn Ala Pro Thr His Thr  
500 505 510

Val His His Tyr Trp Arg Arg Phe Asp Asp Tyr Phe Met Arg Pro Val  
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<211> 1623

<212> DNA

<213> Zea mays

<400> 9

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taa						1623

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 <211> 540  
 <212> PRT  
 <213> Zea mays

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Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg  
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Trp Val Asn Glu Ser Thr Ala Leu Ile Val Gly Leu Gly Thr Gly Thr  
 50 55 60

Val Ile Leu Met Ile Ser Arg Gly Val Val Ile His Val Leu Val Phe  
 65 70 75 80

Ser Glu Asp Leu Phe Phe Phe Tyr Leu Leu Pro Pro Ile Ile Phe Asn  
 85 90 95

Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr  
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Ile Thr Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Thr Val Ile

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Ser	Leu	Gly	Ala	Leu	Gly	Leu	Ile	Ser	Arg	Leu	Asn	Ile	Gly	Ala	Leu
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Glu	Leu	Gly	Asp	Tyr	Leu	Ala	Leu	Gly	Ala	Ile	Phe	Ser	Ala	Thr	Asp
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Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Ser	Gln	Asp	Glu	Thr	Pro	Phe	Leu
				165					170					175	
Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val
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Val	Val	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Ile	Thr	His	Ile	Asp	Ala
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210						215					220				
Ser	Thr	Val	Leu	Gly	Val	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Leu	Val	Ile
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Lys	Lys	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu
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Met	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe	Ala
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Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Gly	Cys	Ile	Val	Met	Ser	His
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Tyr	Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Ile	Thr	Thr	Lys	His
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Thr	Pro	Gly	Lys	Ser	Leu	Ala	Ile	Ser	Ser	Ile	Leu	Met	Gly	Leu	Val
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Met	Val	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn
		355				360						365			
Leu	Ala	Lys	Lys	Thr	Glu	His	Glu	Lys	Ile	Ser	Trp	Lys	Gln	Gln	Val
		370				375					380				
Val	Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu
385					390					395					400
Ala	Tyr	Lys	Lys	Phe	Thr	Arg	Ala	Gly	His	Thr	Gln	Val	Arg	Gly	Asn
				405					410					415	
Ala	Ile	Met	Ile	Thr	Ser	Thr	Ile	Ile	Val	Val	Leu	Phe	Ser	Thr	Met

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Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro His		
435	440	445
Arg Asn Ala Thr Ser Met Leu Ser Asp Asp Ser Ser Pro Lys Ser Leu		
450	455	460
His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Asp Leu Glu Glu Pro		
465	470	475
Thr Asn Ile Pro Arg Pro Ser Ser Ile Arg Gly Glu Phe Leu Thr Met		
485	490	495
Thr Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Ala Phe Met		
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Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser		
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 <212> DNA  
 <213> Zea mays

<400> 11

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<400> 12

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Leu	Leu	Cys	Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg
		35					40					45			
Met	Val	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Leu	Val	Gly	Leu	Gly	Thr	Gly
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Thr	Val	Ile	Leu	Met	Ile	Ser	Arg	Gly	Val	Ser	Ile	His	Val	Leu	Val
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Phe	Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe
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Asn	Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Ile
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Thr	Ile	Ile	Leu	Phe	Gly	Ala	Ile	Gly	Thr	Leu	Ile	Ser	Phe	Val	Ile
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Leu	Glu	Leu	Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala	Thr
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Asp	Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu
			165						170					175	
Leu	Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser
			180					185					190		
Ile	Val	Val	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Ile	Thr	His	Ile	Asn
		195					200					205			
Ala	Glu	Val	Val	Phe	His	Leu	Leu	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Leu
	210					215					220				
Leu	Ser	Thr	Val	Leu	Gly	Val	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Leu	Val
225					230					235					240
Ile	Lys	Lys	Ile	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala
			245						250					255	
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<400> 13
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<210> 14
<211> 539
<212> PRT
<213> Zea mays

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<400> 14
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Cys Leu Cys Leu Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Val
35          40          45

Asn Glu Ser Ile Thr Ala Ile Leu Val Gly Ala Ala Thr Gly Thr Val
50          55          60

Ile Leu Leu Ile Ser Lys Gly Lys Ser Ser His Ile Leu Val Phe Asp
65          70          75          80

Glu Glu Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
85          90          95

Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr Ile
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Ile Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Phe Val Ile Ile Ser

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Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Leu	Leu	Tyr
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Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val
			180					185					190		
Leu	Phe	Asn	Ala	Val	Gln	Lys	Ile	Asp	Phe	Glu	His	Leu	Thr	Gly	Glu
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Val	Ala	Leu	Gln	Val	Phe	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Ser	Thr	Ser
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Thr	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Thr	Arg	Glu	Leu	Ala	Ile	Met
			245						250					255	
Val	Leu	Met	Ala	Tyr	Leu	Ser	Phe	Met	Leu	Ala	Glu	Leu	Phe	Ser	Leu
		260						265					270		
Ser	Gly	Ile	Ile	Thr	Val	Phe	Phe	Cys	Gly	Val	Leu	Met	Ser	His	Val
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Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Ile	Thr	Ser	Arg	His	Val
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Phe	Ala	Met	Leu	Ser	Phe	Ile	Ala	Glu	Thr	Phe	Leu	Phe	Leu	Tyr	Val
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Gly	Thr	Asp	Ala	Leu	Asp	Phe	Thr	Lys	Trp	Lys	Thr	Ser	Ser	Leu	Ser
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Phe	Gly	Lys	Ser	Leu	Gly	Val	Ser	Ser	Val	Leu	Leu	Gly	Leu	Val	Leu
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Val	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	Leu
		355					360					365			
Ser	Lys	Lys	His	Pro	Gly	Glu	Lys	Ile	Thr	Ile	Arg	Gln	Gln	Val	Val
	370					375					380				
Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Ile	Ala	Leu	Ala
385					390					395					400
Phe	Asn	Lys	Phe	Thr	Arg	Ala	Gly	His	Thr	Gln	Val	Arg	Gly	Asn	Ala
			405						410					415	
Ile	Met	Ile	Thr	Ser	Thr	Ile	Ile	Val	Val	Leu	Phe	Ser	Thr	Val	Val

420

425

430

Phe Gly Leu Leu Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro His Arg  
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Asn Ala Thr Ser Met Leu Ser Asp Asp Ser Ser Pro Lys Ser Leu His  
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Ser Pro Leu Leu Thr Ser Gln Leu Ile Ser Ser Ile Glu Glu Pro Thr  
465 470 475 480

Gln Ile Pro Arg Pro Thr Asn Ile Arg Gly Glu Phe Met Thr Met Thr  
485 490 495

Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Lys Phe Met Arg  
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Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro  
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Thr Glu Arg Ser Ser Pro Asp Leu Ser Lys Ala  
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&lt;210&gt; 15

&lt;211&gt; 1617

&lt;212&gt; DNA

&lt;213&gt; Zea mays

&lt;400&gt; 15

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<210> 16  
<211> 538  
<212> PRT  
<213> Zea mays

<400> 16

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Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp	Leu	Asn
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Glu	Ser	Ile	Thr	Ala	Leu	Ile	Ile	Gly	Leu	Gly	Thr	Gly	Val	Val	Ile
	50					55					60				
Leu	Leu	Ile	Ser	Arg	Gly	Lys	Asn	Ser	Arg	Leu	Leu	Val	Phe	Ser	Glu
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Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn	Ala	Gly
				85					90					95	
Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Met	Thr	Ile	Thr
			100					105					110		
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Cys	Thr	Leu	Gln	Val	Leu	His	Gln	Asp	Glu	Thr	Pro	Phe	Leu	Tyr	Ser
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Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Leu
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Phe	Asn	Ala	Val	Gln	Lys	Ile	Gln	Phe	Thr	His	Ile	Asn	Ala	Trp	Thr
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Ala	Leu	Gln	Leu	Ile	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Ser	Thr	Ser	Thr
	210					215					220				
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225					230					235					240
Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Thr	Arg	Glu	Leu	Ala	Ile	Met	Ile
				245					250					255	
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 Trp His Asn Val Thr Glu Ser Ser Arg Thr Thr Ser Arg His Val Phe  
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 Ala Thr Leu Ser Phe Ile Ser Glu Thr Phe Ile Phe Leu Tyr Val Gly  
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 Met Asp Ala Leu Asp Phe Glu Lys Trp Lys Thr Ser Ser Leu Ser Phe  
 325 330 335  
 Gly Gly Thr Leu Gly Val Ser Gly Val Leu Met Gly Leu Val Met Leu  
 340 345 350  
 Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala  
 355 360 365  
 Lys Lys His Gln Ser Glu Lys Ile Ser Phe Arg Met Gln Val Val Ile  
 370 375 380  
 Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Leu  
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 Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala Ile  
 405 410 415  
 Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val Phe  
 420 425 430  
 Gly Met Ile Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser Gly  
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 His Pro Arg Glu Leu Ser Glu Pro Ser Ser Pro Lys Ser Phe His Ser  
 450 455 460  
 Pro Leu Leu Thr Ser Gln Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn  
 465 470 475 480  
 Ile Val Arg Pro Ser Ser Leu Arg Gly Leu Leu Thr Lys Pro Thr His  
 485 490 495  
 Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro  
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<210> 17

<211> 2564

<212> DNA

<213> Hordeum vulgare

<400> 17

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<210> 18

<211> 538

<212> PRT

<213> Hordeum vulgare

<400> 18

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			20					25					30		

Ala	Leu	Leu	Cys	Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn
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Gly	Val	Val	Ile	Leu	Met	Thr	Thr	Lys	Gly	Lys	Ser	Ser	His	Val	Leu
65					70					75					80
Val	Phe	Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile
				85					90					95	
Phe	Asn	Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe
			100					105					110		
Met	Thr	Ile	Thr	Leu	Phe	Gly	Ala	Val	Gly	Thr	Met	Ile	Ser	Phe	Phe
		115					120					125			
Thr	Ile	Ser	Leu	Ala	Ala	Ile	Ala	Ile	Phe	Ser	Lys	Met	Asn	Ile	Gly
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385	390	395
Ala Leu Ala Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His		
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Gly Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser		
420	425	430
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 <213> Triticum aestivum

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 Arg Trp Leu Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr  
 50 55 60  
 Gly Val Val Ile Leu Met Thr Thr Lys Gly Lys Ser Ser His Val Leu  
 65 70 75 80  
 Val Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile  
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 Phe Asn Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe  
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 Met Ala Ile Thr Leu Phe Gly Ala Val Gly Thr Met Met Ser Phe Phe

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Thr	Asp	Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro
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Phe	Leu	Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr
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Ser	Val	Val	Leu	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Pro	Asn	Gln	Ile
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Ala	Leu	Val	Met	Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu
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Ala	Leu	Ala	Tyr	Asn	Lys	Phe	Thr	Arg	Ser	Gly	His	Thr	Gln	Leu	His
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420

425

430

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Pro Ala Ser Ser Asn Gly Ala Ala Ser Asp Pro Ala Ser Pro Lys Ser  
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Leu His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Asp Leu Glu Ala  
 465 470 475 480

Pro Leu Pro Ile Val Arg Pro Ser Ser Leu Arg Met Leu Ile Thr Lys  
 485 490 495

Pro Thr His Thr Ile His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu  
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Met Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Tyr Ser Pro Gly  
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Ser Pro Thr Asp Pro Asn Val Leu Val Glu  
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&lt;210&gt; 21

&lt;211&gt; 1726

&lt;212&gt; DNA

&lt;213&gt; Oryza sativa

&lt;400&gt; 21

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1726

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 <212> DNA  
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<400> 23

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gacgagtttg	atatagaggc	tccaagggcg	ataaatttat	tgaacggtag	ttctattcag	1560
acagatttgg	gcccataatc	tgacaacaat	tctccagata	tttcaattga	ccaattcgcg	1620
gtcagcagta	acaagaatct	ccccaataac	atatccacaa	ctggtggtaa	tacttttgga	1680
ggccttaatg	aaactgagaa	tactagccct	aaccgcgcaa	ggtcttctat	ggataagcgt	1740
aatttgagag	ataaactggg	aacaatctff	aattccgact	cacaatgggt	tcaaaatfff	1800
gatgaacagg	tattgaagcc	agtattcttg	gacaacgtff	ctccatcctt	acaagattcg	1860
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<210> 24

<211> 633

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

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Thr	Ala	Lys	Arg	Ala	Val	Asp	Pro	Asp	Asp	Asp	Asp	Glu	Leu	Leu	Pro
			20					25					30		
Ser	Pro	Asp	Leu	Pro	Gly	Ser	Asp	Asp	Pro	Ile	Ala	Gly	Asp	Pro	Asp
		35					40					45			
Val	Asp	Leu	Asn	Pro	Val	Thr	Glu	Glu	Met	Phe	Ser	Ser	Trp	Ala	Leu
	50					55					60				
Phe	Ile	Met	Leu	Leu	Leu	Leu	Ile	Ser	Ala	Leu	Trp	Ser	Ser	Tyr	Tyr
65				70					75					80	
Leu	Thr	Gln	Lys	Arg	Ile	Arg	Ala	Val	His	Glu	Thr	Val	Leu	Ser	Ile

85

90

95

Phe Tyr Gly Met Val Ile Gly Leu Ile Ile Arg Met Ser Pro Gly His  
 100 105 110

Tyr Ile Gln Asp Thr Val Thr Phe Asn Ser Ser Tyr Phe Phe Asn Val  
 115 120 125

Leu Leu Pro Pro Ile Ile Leu Asn Ser Gly Tyr Glu Leu Asn Gln Val  
 130 135 140

Asn Phe Phe Asn Asn Met Leu Ser Ile Leu Ile Phe Ala Ile Pro Gly  
 145 150 155 160

Thr Phe Ile Ser Ala Val Val Ile Gly Ile Ile Leu Tyr Ile Trp Thr  
 165 170 175

Phe Leu Gly Leu Glu Ser Ile Asp Ile Ser Phe Ala Asp Ala Met Ser  
 180 185 190

Val Gly Ala Thr Leu Ser Ala Thr Asp Pro Val Thr Ile Leu Ser Ile  
 195 200 205

Phe Asn Ala Tyr Lys Val Asp Pro Lys Leu Tyr Thr Ile Ile Phe Gly  
 210 215 220

Glu Ser Leu Leu Asn Asp Ala Ile Ser Ile Val Met Phe Glu Thr Cys  
 225 230 235 240

Gln Lys Phe His Gly Gln Pro Ala Thr Phe Ser Ser Val Phe Glu Gly  
 245 250 255

Ala Gly Leu Phe Leu Met Thr Phe Ser Val Ser Leu Leu Ile Gly Val  
 260 265 270

Leu Ile Gly Ile Leu Val Ala Leu Leu Leu Lys His Thr His Ile Arg  
 275 280 285

Arg Tyr Pro Gln Ile Glu Ser Cys Leu Ile Leu Leu Ile Ala Tyr Glu  
 290 295 300

Ser Tyr Phe Phe Ser Asn Gly Cys His Met Ser Gly Ile Val Ser Leu  
 305 310 315 320

Leu Phe Cys Gly Ile Thr Leu Lys His Tyr Ala Tyr Tyr Asn Met Ser  
 325 330 335

Arg Arg Ser Gln Ile Thr Ile Lys Tyr Ile Phe Gln Leu Leu Ala Arg  
 340 345 350

Leu Ser Glu Asn Phe Ile Phe Ile Tyr Leu Gly Leu Glu Leu Phe Thr  
 355 360 365

Glu Val Glu Leu Val Tyr Lys Pro Leu Leu Ile Ile Val Ala Ala Ile  
 370 375 380

Ser Ile Cys Val Ala Arg Trp Cys Ala Val Phe Pro Leu Ser Gln Phe

385		390		395		400
Val Asn Trp Ile Tyr Arg Val Lys Thr Ile Arg Ser Met Ser Gly Ile	405		410		415	
Thr Gly Glu Asn Ile Ser Val Pro Asp Glu Ile Pro Tyr Asn Tyr Gln	420		425		430	
Met Met Thr Phe Trp Ala Gly Leu Arg Gly Ala Val Gly Val Ala Leu	435		440		445	
Ala Leu Gly Ile Gln Gly Glu Tyr Lys Phe Thr Leu Leu Ala Thr Val	450		455		460	
Leu Val Val Val Val Leu Thr Val Ile Ile Phe Gly Gly Thr Thr Ala	465		470		475	480
Gly Met Leu Glu Val Leu Asn Ile Lys Thr Gly Cys Ile Ser Glu Glu	485		490		495	
Asp Thr Ser Asp Asp Glu Phe Asp Ile Glu Ala Pro Arg Ala Ile Asn	500		505		510	
Leu Leu Asn Gly Ser Ser Ile Gln Thr Asp Leu Gly Pro Tyr Ser Asp	515		520		525	
Asn Asn Ser Pro Asp Ile Ser Ile Asp Gln Phe Ala Val Ser Ser Asn	530		535		540	
Lys Asn Leu Pro Asn Asn Ile Ser Thr Thr Gly Gly Asn Thr Phe Gly	545		550		555	560
Gly Leu Asn Glu Thr Glu Asn Thr Ser Pro Asn Pro Ala Arg Ser Ser	565		570		575	
Met Asp Lys Arg Asn Leu Arg Asp Lys Leu Gly Thr Ile Phe Asn Ser	580		585		590	
Asp Ser Gln Trp Phe Gln Asn Phe Asp Glu Gln Val Leu Lys Pro Val	595		600		605	
Phe Leu Asp Asn Val Ser Pro Ser Leu Gln Asp Ser Ala Thr Gln Ser	610		615		620	
Pro Ala Asp Phe Ser Ser Gln Asn His	625		630			

<210> 25

<211> 1857

<212> DNA

<213> Magnaporthe grisea

<400> 25

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gacctcgtca gcttcgatta ccaaattctt ttcaacctcc tccttccacc catcatcctc	180
tcgtccgggt acgagttaca tcaggccaac ttcttccggc acatcggaac aattctcacg	240



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actttgtcag	ctaccgatcc	tgtcaccatc	atagccatct	tcaactcgta	caaggtggac	420
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ggggcgcttc	ttggcatcct	caccgcgctc	atgctcaagt	acacgtacct	caggagggtt	660
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gccatacaca	tgtctggaat	tgtgtcactg	ttgttctgcg	gaatcacact	caaacactat	780
gcatacttca	acatgtcgcg	aagaactcag	cttacgacca	agtacatgtt	ccaggtcctc	840
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tgggttgccg	tattcccact	ctcgtgggcc	atcaactggg	tccacaagta	ccgggcagaa	1020
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accgaggacc	caacagccct	gttcaggcag	ctggacgagg	actacatcaa	accgaagcta	1800
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<210> 26

<211> 618

<212> PRT

<213> Magnaporthe grisea

<400> 26

Met	Thr	Phe	Asp	Ile	Ala	Gly	Asn	Leu	Leu	Glu	Leu	Thr	Arg	Arg	Ala
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	20							25				30			

Val	Phe	Ala	Val	Asp	Gly	Leu	Gln	Asp	Leu	Val	Ser	Phe	Asp	Tyr	Gln
	35					40					45				

Ile	Phe	Phe	Asn	Leu	Leu	Leu	Pro	Pro	Ile	Ile	Leu	Ser	Ser	Gly	Tyr
	50				55						60				

Glu	Leu	His	Gln	Ala	Asn	Phe	Phe	Arg	His	Ile	Gly	Thr	Ile	Leu	Thr
65				70						75				80	

Phe	Ala	Phe	Ala	Gly	Thr	Phe	Leu	Ser	Ala	Val	Val	Ile	Gly	Val	Ile
			85						90					95	

Leu	Trp	Leu	Tyr	Thr	Arg	Val	Pro	Leu	Glu	Gly	Leu	Thr	Met	Asn	Trp
		100						105					110		

Ile	Asp	Ala	Ile	Ser	Val	Gly	Ala	Thr	Leu	Ser	Ala	Thr	Asp	Pro	Val
	115						120					125			

Thr	Ile	Ile	Ala	Ile	Phe	Asn	Ser	Tyr	Lys	Val	Asp	Pro	Lys	Leu	Tyr	130	135	140	
Thr	Ile	Ile	Phe	Gly	Glu	Ala	Ile	Leu	Asn	Asp	Ala	Val	Ala	Ile	Val	145	150	155	160
Ile	Phe	Glu	Ser	Ala	Gln	Lys	Ser	Ala	Arg	Gly	Leu	Thr	Lys	Gly	Ser	165	170	175	
Ala	Ala	Gly	Ile	Ser	Thr	Phe	Phe	Trp	Gly	Phe	Trp	Ile	Phe	Leu	Arg	180	185	190	
Asp	Phe	Phe	Gly	Ser	Leu	Phe	Ile	Gly	Ala	Leu	Leu	Gly	Ile	Leu	Thr	195	200	205	
Ala	Leu	Met	Leu	Lys	Tyr	Thr	Tyr	Leu	Arg	Arg	Phe	Pro	Lys	Leu	Glu	210	215	220	
Ser	Cys	Leu	Ile	Val	Leu	Ile	Ala	Tyr	Ala	Thr	Tyr	Tyr	Phe	Ser	Gln	225	230	235	240
Ala	Ile	His	Met	Ser	Gly	Ile	Val	Ser	Leu	Leu	Phe	Cys	Gly	Ile	Thr	245	250	255	
Leu	Lys	His	Tyr	Ala	Tyr	Phe	Asn	Met	Ser	Arg	Arg	Thr	Gln	Leu	Thr	260	265	270	
Thr	Lys	Tyr	Met	Phe	Gln	Val	Leu	Ala	Gln	Leu	Ser	Glu	Asn	Phe	Ile	275	280	285	
Phe	Ile	Tyr	Leu	Gly	Val	Ser	Leu	Phe	Thr	Asp	Lys	Asp	Leu	Gln	Phe	290	295	300	
Gln	Pro	Leu	Leu	Ile	Ile	Val	Thr	Val	Met	Ala	Val	Cys	Ala	Ala	Arg	305	310	315	320
Trp	Val	Ala	Val	Phe	Pro	Leu	Ser	Trp	Ala	Ile	Asn	Trp	Phe	His	Lys	325	330	335	
Tyr	Arg	Ala	Glu	Arg	Arg	Gly	Ile	Lys	Asn	Val	Pro	Glu	Glu	Leu	Pro	340	345	350	
Tyr	Lys	Tyr	Gln	Gly	Met	Leu	Phe	Trp	Ala	Gly	Leu	Arg	Gly	Ala	Val	355	360	365	
Gly	Val	Ala	Leu	Ala	Ala	Leu	Leu	Thr	Ala	Lys	Asp	His	Arg	Ala	Phe	370	375	380	
Lys	Ala	Thr	Val	Leu	Val	Val	Val	Val	Leu	Thr	Val	Ile	Ile	Phe	Gly	385	390	395	400
Gly	Thr	Thr	Val	Asn	Val	Leu	Glu	Ile	Leu	Glu	Ile	Arg	Thr	Gly	Val	405	410	415	
Thr	Asp	Glu	Ile	Asp	Ser	Asp	Asp	Glu	Phe	Asp	Ile	Glu	Ala	Val	Gly	420	425	430	

Gly Tyr Tyr Lys Arg Ser Gly Asn Gly Ile Gly Tyr Ser Pro Ala Gly  
 435 440 445  
 Arg Asn Gly Val Val Pro Leu Asp Thr Arg Pro Gly Arg Arg Arg Asp  
 450 455 460  
 Ser Asn Gly Ala Val Gly Gly Arg Asp Ala Ser Gly Trp Ser Ser Gly  
 465 470 475 480  
 His Arg Ser Pro Leu Ser Ala Ala Arg Pro Gly Ser Leu Val Arg Thr  
 485 490 495  
 Gly Ser Thr Arg Glu Glu Ala Glu Arg Leu Asp Leu Leu Gly Asn Pro  
 500 505 510  
 Gly Gly Ser Thr Asp Ser Asp Asp Phe Gly Ser Asp Ile Asp Thr Ser  
 515 520 525  
 Asp Leu Pro Pro Pro Ala Pro Arg Arg Arg Ser Ser Pro Met Pro Pro  
 530 535 540  
 Thr Gly Asp Glu Glu Ala Ala Gly Leu Pro Ala Gly Gly Ser Arg Thr  
 545 550 555 560  
 Arg Ser Asn Thr Glu Thr Gly Gly Leu Ser Ala Thr Ala Ala Ile Arg  
 565 570 575  
 Gln Leu Phe Ser Thr Glu Asp Pro Thr Ala Leu Phe Arg Gln Leu Asp  
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 595 600 605  
 Gly Asn Gly Gly Gly Ala Gly Gly Ser Ser  
 610 615

<210> 27  
 <211> 654  
 <212> DNA  
 <213> *Oryza sativa*

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 ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac 180  
 aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgtttttatt 240  
 attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt 300  
 gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat 360  
 ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc tttgctaccc 420  
 atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag 480  
 gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt 540  
 aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa 600  
 aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agta 654

<210> 28

<211> 941  
 <212> DNA  
 <213> *Oryza sativa*

<400> 28  
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 ataatctata gtactacaat aatatcagtg tTTtagagaa tcatataaat gaacagttag 180  
 acatggTcta aaggacaatt gagtattTTg acaacaggac tctacagTTt tatcTTTTta 240  
 gtgtgcatgt gTTctcTTt tTTTTgcaa atagcTTcac ctatataata cTTcatccat 300  
 Tttattagta catccattta gggTTtaggg ttaatggTTt ttatagacta atTTTTTTtag 360  
 tacatctatt ttattctatt ttagcctcta aattaagaaa actaaaactc tattTTtagtt 420  
 TTTTTattta ataatttaga tataaaaatag aataaaaataa agtgactaaa aattaaacaa 480  
 ataccctTTa agaaattaaa aaaactaagg aaacattTTt cttgTTTcga gtagataatg 540  
 ccagcctgtt aaacgccgtc gacgagtcta acggacacca accagcgaac cagcagcgtc 600  
 gcgtcgggcc aagcgaagca gacggcacgg catctctgtc gctgcctctg gaccctctc 660  
 gagagtTccg ctccaccgtt ggacttgctc cgctgtcggc atccagaaat tgcgtggcgg 720  
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<210> 29  
 <211> 50  
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<220>  
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<400> 29  
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<210> 30  
 <211> 48  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer: prm3123

<400> 30  
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